

S.Liu

Re-run



1653

RAW SEQUENCE LISTING

DATE: 03/15/2002

PATENT APPLICATION: US/09/773,877B

TIME: 16:23:54

Input Set : N:\Crf3\Refhold\I773877B.raw

Output Set: N:\CRF3\03152002\I773877B.raw

1 <110> APPLICANT: Xia, Yu-Ping et al.
 2 <120> TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
 3 <130> FILE REFERENCE: REG 710b
 C--> 4 <140> CURRENT APPLICATION NUMBER: US/09/773,877B
 5 <141> CURRENT FILING DATE: 2001-01-31
 6 <160> NUMBER OF SEQ ID NOS: 27
 7 <170> SOFTWARE: PatentIn version 3.0
 9 <210> SEQ ID NO: 1
 10 <211> LENGTH: 36
 11 <212> TYPE: DNA
 12 <213> ORGANISM: Artificial Sequence
 13 <220> FEATURE:
 14 <223> OTHER INFORMATION: Primer
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 37 <211> LENGTH: 38
 38 <212> TYPE: DNA
 39 <213> ORGANISM: Artificial Sequence
 40 <220> FEATURE:
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 45 <210> SEQ ID NO: 5
 46 <211> LENGTH: 36
 47 <212> TYPE: DNA
 48 <213> ORGANISM: Artificial Sequence

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50 <223> OTHER INFORMATION: Primer
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57 <213> ORGANISM: Artificial Sequence
58 <220> FEATURE:
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65 <212> TYPE: DNA
66 <213> ORGANISM: Artificial Sequence
67 <220> FEATURE:
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73 <211> LENGTH: 39
74 <212> TYPE: DNA
75 <213> ORGANISM: Artificial Sequence
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103 <220> FEATURE:

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104 <223> OTHER INFORMATION: Flt1(1-3)-Fc
105 <221> NAME/KEY: CDS
106 <222> LOCATION: (1)..(1704)
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110      1                               5                               10                               15
111      tgt ctg ctt ctc aca gga tct agt tca ggt tca aaa tta aaa gat cct      96
112      Cys Leu Leu Leu Thr Gly Ser Ser Gly Ser Lys Leu Lys Asp Pro
113      20                               25                               30
114      gaa ctg agt tta aaa ggc acc cag cac atc atg caa gca ggc cag aca      144
115      Glu Leu Ser Leu Lys Gly Thr Gln His Ile Met Gln Ala Gly Gln Thr
116      35                               40                               45
117      ctg cat ctc caa tgc agg ggg gaa gca gcc cat aaa tgg tct ttg cct      192
118      Leu His Leu Gln Cys Arg Gly Glu Ala Ala His Lys Trp Ser Leu Pro
119      50                               55                               60
120      gaa atg gtg agt aag gaa agc gaa agg ctg agc ata act aaa tct gcc      240
121      Glu Met Val Ser Lys Glu Ser Glu Arg Leu Ser Ile Thr Lys Ser Ala
122      65                               70                               75                               80
123      tgt gga aga aat ggc aaa caa ttc tgc agt act tta acc ttg aac aca      288
124      Cys Gly Arg Asn Gly Lys Gln Phe Cys Ser Thr Leu Thr Leu Asn Thr
125      85                               90                               95
126      gct caa gca aac cac act ggc ttc tac agc tgc aaa tat cta gct gta      336
127      Ala Gln Ala Asn His Thr Gly Phe Tyr Ser Cys Lys Tyr Leu Ala Val
128      100                              105                              110
129      cct act tca aag aag aag gaa aca gaa tct gca atc tat ata ttt att      384
130      Pro Thr Ser Lys Lys Lys Glu Thr Glu Ser Ala Ile Tyr Ile Phe Ile
131      115                              120                              125
132      agt gat aca ggt aga cct ttc gta gag atg tac agt gaa atc ccc gaa      432
133      Ser Asp Thr Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile Pro Glu
134      130                              135                              140
135      att ata cac atg act gaa gga agg gag ctc gtc att ccc tgc cgg gtt      480
136      Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val
137      145                              150                              155                              160
138      acg tca cct aac atc act gtt act tta aaa aag ttt cca ctt gac act      528
139      Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr
140      165                              170                              175
141      ttg atc cct gat gga aaa cgc ata atc tgg gac agt aga aag ggc ttc      576
142      Leu Ile Pro Asp Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe
143      180                              185                              190
144      atc ata tca aat gca acg tac aaa gaa ata ggg ctt ctg acc tgt gaa      624
145      Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile Gly Leu Leu Thr Cys Glu
146      195                              200                              205
147      gca aca gtc aat ggg cat ttg tat aag aca aac tat ctc aca cat cga      672
148      Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg
149      210                              215                              220
150      caa acc aat aca atc ata gat gtc caa ata agc aca cca cgc cca gtc      720
151      Gln Thr Asn Thr Ile Ile Asp Val Gln Ile Ser Thr Pro Arg Pro Val
152      225                              230                              235                              240

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153	aaa tta ctt aga ggc cat act ctt gtc ctc aat tgt act gct acc act	768
154	Lys Leu Leu Arg Gly His Thr Leu Val Leu Asn Cys Thr Ala Thr Thr	
155	245 250 255	
156	ccc ttg aac acg aga gtt caa atg acc tgg agt tac cct gat gaa aaa	816
157	Pro Leu Asn Thr Arg Val Gln Met Thr Trp Ser Tyr Pro Asp Glu Lys	
158	260 265 270	
159	aat aag aga gct tcc gta agg cga cga att gac caa agc aat tcc cat	864
160	Asn Lys Arg Ala Ser Val Arg Arg Ile Asp Gln Ser Asn Ser His	
161	275 280 285	
162	gcc aac ata ttc tac agt gtt ctt act att gac aaa atg cag aac aaa	912
163	Ala Asn Ile Phe Tyr Ser Val Leu Thr Ile Asp Lys Met Gln Asn Lys	
164	290 295 300	
165	gac aaa gga ctt tat act tgt cgt gta agg agt gga cca tca ttc aaa	960
166	Asp Lys Gly Leu Tyr Thr Cys Arg Val Arg Ser Gly Pro Ser Phe Lys	
167	305 310 315 320	
168	tct gtt aac acc tca gtg cat ata tat gat aaa gca ggc ccg ggc gag	1008
169	Ser Val Asn Thr Ser Val His Ile Tyr Asp Lys Ala Gly Pro Gly Glu	
170	325 330 335	
171	ccc aaa tct tgt gac aaa act cac aca tgc cca ccg tgc cca gca cct	1056
172	Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro	
173	340 345 350	
174	gaa ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag	1104
175	Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys	
176	355 360 365	
177	gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg	1152
178	Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val	
179	370 375 380	
180	gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac	1200
181	Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp	
182	385 390 395 400	
183	ggc gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac	1248
184	Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr	
185	405 410 415	
186	aac agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac	1296
187	Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp	
188	420 425 430	
189	tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc	1344
190	Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu	
191	435 440 445	
192	cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga	1392
193	Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg	
194	450 455 460	
195	gaa cca cag gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag	1440
196	Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys	
197	465 470 475 480	
198	aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac	1488
199	Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp	
200	485 490 495	
201	atc gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac aag	1536

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202   Ile Ala Val  Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
203           500                      505                      510
204   acc acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc      1584
205   Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
206           515                      520                      525
207   aag ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca      1632
208   Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
209           530                      535                      540
210   tgc tcc gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc      1680
211   Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
212           545                      550                      555                      560
213   ctc tcc ctg tct ccg ggt aaa tga      1704
214   Leu Ser Leu Ser Pro Gly Lys
215           565
217 <210> SEQ ID NO: 12
218 <211> LENGTH: 567
219 <212> TYPE: PRT
220 <213> ORGANISM: Artificial Sequence
221 <220> FEATURE:
222 <223> OTHER INFORMATION: Flt(1-3)-Fc
223 <400> SEQUENCE: 12
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226   Cys Leu Leu Leu Thr Gly Ser Ser Ser Gly Ser Lys Leu Lys Asp Pro
227           20           25           30
228   Glu Leu Ser Leu Lys Gly Thr Gln His Ile Met Gln Ala Gly Gln Thr
229           35           40           45
230   Leu His Leu Gln Cys Arg Gly Glu Ala Ala His Lys Trp Ser Leu Pro
231           50           55           60
232   Glu Met Val Ser Lys Glu Ser Glu Arg Leu Ser Ile Thr Lys Ser Ala
233           65           70           75           80
234   Cys Gly Arg Asn Gly Lys Gln Phe Cys Ser Thr Leu Thr Leu Asn Thr
235           85           90           95
236   Ala Gln Ala Asn His Thr Gly Phe Tyr Ser Cys Lys Tyr Leu Ala Val
237           100          105          110
238   Pro Thr Ser Lys Lys Lys Glu Thr Glu Ser Ala Ile Tyr Ile Phe Ile
239           115          120          125
240   Ser Asp Thr Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile Pro Glu
241           130          135          140
242   Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val
243           145          150          155          160
244   Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr
245           165          170          175
246   Leu Ile Pro Asp Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe
247           180          185          190
248   Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile Gly Leu Leu Thr Cys Glu
249           195          200          205
250   Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg
251           210          215          220

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L:4 M:270 C: Current Application Number differs, Wrong Format